Appl. No. 09/381,480
Amdt. dated September 30, 2004
Reply to Office Action dated April 30, 2004

PATENT

Amendments to the Specification:

In the specification 16, p. 7, line 35 - please rewrite the paragraph as follows:

Reference sequences for polymorphic site identification are often obtained from computer databases such as Genbank, the Stanford Genome Center, The Institute for Genome Research and the Whitehead Institute. The latter databases are available at ~~http://www~~ world wide web genome.wi.mit.edu; ~~http://~~ world wide web shgc.stanford.edu and ~~http://ww.~~ world wide web tigr.org. Reference sequences are typically from well-characterized organisms, such as human, mouse, *C. elegans*, *arabidopsis*, *drosophila*, yeast, *E. coli* or *Bacillus subtilis*. A reference sequence can vary in length from 5 bases to at least 1,000,000 bases. References sequences are often of the order of 100-10,000 bases. The reference sequence can be from expressed or nonexpressed regions of the genome. In some methods, in which RNA samples are used, highly expressed reference sequences are sometimes preferred to avoid the need for RNA amplification. The function of a reference sequence may or may not be known. Reference sequences can also be from episomes such as mitochondrial DNA. Of course, multiple reference sequences can be analyzed independently.